

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/663,451

DATE: 09/24/2003
TIME: 15:32:21

Input Set : N:\Crf3\RULE60\US10663451.raw.txt
Output Set: N:\CRF4\09242003\J663451.raw

49	Ser Lys Lys Lys Asn Val Thr Met Arg Ser Ile Lys Thr Thr Arg	
50	40 45 50	
51	gac cga gtg cct aca tat cag tac aac atg aat ttt gaa aag ctg ggc	247
52	Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe Glu Lys Leu Gly	
53	55 60 65	
54	aaa tgc atc ata ata aac aac aag aac ttt gat aaa gtg aca ggt atg	295
55	Lys Cys Ile Ile Asn Asn Lys Asn Phe Asp Lys Val Thr Gly Met	
56	70 75 80	
57	ggc gtt cga aac gga aca gac aaa gat gcc gag gcg ctc ttc aag tgc	343
58	Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala Leu Phe Lys Cys	
59	85 90 95 100	
60	tgc cga agc ctg ggt ttt gac gtg att gtc tat aat gac tgc tct tgt	391
61	Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn Asp Cys Ser Cys	
62	105 110 115	
63	gcc aag atg caa gat ctg ctt aaa aaa gct tct gaa gag gac cat aca	439
64	Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu Glu Asp His Thr	
65	120 125 130	
66	aat gcc gcc tgc ttc gcc tgc atc ctc tta agc cat gga gaa gaa aat	487
67	Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His Gly Glu Glu Asn	
68	135 140 145	
69	gta att tat ggg aaa gat ggt gtc aca cca ata aag gat ttg aca gcc	535
70	Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys Asp Leu Thr Ala	
71	150 155 160	
72	cac ttt agg ggg gat aga tgc aaa acc ctt tta gag aaa ccc aaa ctc	583
73	His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu Lys Pro Lys Leu	
74	165 170 175 180	
75	tgc ttc att cag gct tgc cga ggg acc gag ctt gat gat ggc atc cag	631
76	Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp Asp Gly Ile Gln	
77	185 190 195	
78	gcc gac tcg ggg ccc atc aat gac aca gat gct aat cct cga tac aag	679
79	Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn Pro Arg Tyr Lys	
80	200 205 210	
81	atc cca gtg gaa gct gac ttc ctc ttc gcc tat tcc acg gtt cca ggc	727
82	Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser Thr Val Pro Gly	
83	215 220 225	
84	tat tac tcg tgg agg agc cca gga aga ggc tcc tgg ttt gtg caa gcc	775
85	Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp Phe Val Gln Ala	
86	230 235 240	
87	ctc tgc tcc atc ctg gag gag cac gga aaa gac ctg gaa atc atg cag	823
88	Leu Cys Ser Ile Leu Glu Glu His Gly Lys Asp Leu Glu Ile Met Gln	
89	245 250 255 260	
90	atc ctc acc agg gtg aat gac aga gtt gcc agg cac ttt gag tct cag	871
91	Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His Phe Glu Ser Gln	
92	265 270 275	
93	tct gat gac cca cac ttc cat gag aag aag cag atc ccc tgt gtg gtc	919
94	Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile Pro Cys Val Val	
95	280 285 290	
96	tcc atg ctc acc aag gaa ctc tac ttc agt caa tag ccatacagg	965
97	Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln	

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98	295	300	
99	ggtacattct agctgagaag caatgggtca ctcattaatg aatcacattt ttttatgctc	1025	
100	ttgaaatatt cagaaattct ccaggatttt aatttcagga aatgtattt attcaacagg	1085	
101	gaagaaactt tctggtgctg tctttgttc tctgaattt cagagactt tttataatgt	1145	
102	tattcatttgc gtgactgtgt aactttctct taagattaat tttcttgc tatgtctgtt	1205	
103	accttgttaa tagacttaat acatgcaaca gaagtgactt ctggagaaag ctcatggctg	1265	
104	tgtccactgc aattgggtgt aacagtggta gagtcatgtt tgcacttggc aaaaagaatc	1325	
105	ccaatgtttt acaaaacaca gccaaggggg tatttactgc tctttattgc agaatgtggg	1385	
106	tattgagtgt gatttgaatg attttcatt ggcttagggc agatttcat gcaaaagttc	1445	
107	tcatatgagt tagaggagaa aaagcttaat gattctgata tgtatccatc aggatccagt	1505	
108	ctggaaaaca gaaaccattc taggtgtttc aacagaggga gtttaataca ggaattgac	1565	
109	ttacatagat gataaaagag aagccaaaca gcaagaagct gttaccacac ccaggcstat	1625	
110	gaggataatg ggaagaggtt tggtttcctg tgtccagtag tgggatcatc cagaggagct	1685	
111	ggaaccatgg tggggcgtgc ctatggggag ttaggaccac caatggattt tgaaaaatgg	1745	
112	agccatgaca agaacaaggc cactgactga gatggagtga gctgagacag ataagagaat	1805	
113	accttgtc acctatcctg ccctcacatc ttccaccac accttactgc ccagccstat	1865	
114	ctggaaagcca cctcaccaag gacctggaa gagcaaggga cagtggcgg gggaaagaac	1925	
115	aagaaatggg tgtaagcctg gcccataatg tgaacataag taatcactaa tgctcaacaa	1985	
116	tttatccatt caatcattt ttcattgggt tgtcagatag tctatgtatg tgtaaaacaa	2045	
117	tctgtttgg ctttatgtgc aaaatctgtt atagctttaa aatatatctg gaactttta	2105	
118	gattattcca agccttattt ttagtaataat tttgttactt ttagttctat aagtggagaa	2165	
119	gagtttatgg caaagattt tggcactttt tttcaagat ggtgttatct tttgaattct	2225	
120	tgataaatga ctgtttttt ctgcctaata gtaactgggtt aaaaaacaaa tgttcatatt	2285	
121	tattgattaa aaatgtgggt gctt	2309	
123	<210> SEQ ID NO: 4		
124	<211> LENGTH: 26		
125	<212> TYPE: DNA		
126	<213> ORGANISM: Artificial Sequence		
127	<220> FEATURE:		
128	<223> OTHER INFORMATION: PCR Primer		
129	<400> SEQUENCE: 4		
130	attgggtgtt acagtggtag agtcat	26	
132	<210> SEQ ID NO: 5		
133	<211> LENGTH: 20		
134	<212> TYPE: DNA		
135	<213> ORGANISM: Artificial Sequence		
136	<220> FEATURE:		
137	<223> OTHER INFORMATION: PCR Primer		
138	<400> SEQUENCE: 5		
139	cccttggctg tggtttgtca	20	
141	<210> SEQ ID NO: 6		
142	<211> LENGTH: 27		
143	<212> TYPE: DNA		
144	<213> ORGANISM: Artificial Sequence		
145	<220> FEATURE:		
146	<223> OTHER INFORMATION: PCR Probe		
147	<400> SEQUENCE: 6		
148	ttgcacttgg caaaaagaat cccaaatg	27	
150	<210> SEQ ID NO: 7		

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151 <211> LENGTH: 21
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: PCR Primer
156 <400> SEQUENCE: 7
157 caacggattt gggtcgatgg g 21
159 <210> SEQ ID NO: 8
160 <211> LENGTH: 26
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: PCR Primer
165 <400> SEQUENCE: 8
166 ggcaacaata tccactttac cagagt 26
168 <210> SEQ ID NO: 9
169 <211> LENGTH: 21
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: PCR Probe
174 <400> SEQUENCE: 9
175 cgccctggta ccagggtgc t 21
177 <210> SEQ ID NO: 10
178 <211> LENGTH: 2006
179 <212> TYPE: DNA
180 <213> ORGANISM: Mus musculus
181 <220> FEATURE:
182 <221> NAME/KEY: CDS
183 <222> LOCATION: (474)...(1496)
184 <400> SEQUENCE: 10
185 agctcagtga ggctgatgtg tactgcacat ttaaaaaaaaaa aatcacagga attttcatac 60
186 aatgaataaa accacaacaa tacatgtaga attggcaggt ggaaaaagagc cagcaaggc 120
187 tcaaactaat cactcactt ccctcttcag catagttcaa ccaacagtag cacacttca 180
188 cctacaaaatc ttaaaagttagc tccatcaa at ctgcaggttt cacattattt aaaaatgtctg 240
189 tcacataggt acaaattttag aatcatcaca ttatattaca tggttattct aggtcatcta 300
190 tagatcagat cttagactac agtgattgaa gttcttcgta cagccatcaa aaaggcac 360
191 atgatcatta cctactgtta gtcacatct aaaggcatga aaaggttcc ttttttcaa 420
192 ctgaccaaaaa cactttaccc caatagtgcc aggttccctc tctgctgctt tga atg 476
193 Met
194 1
195 ttc aca gcc caa gtg ttc tca gag tcc ttt aca aaa act gag ttg ctg 524
196 Phe Thr Ala Gln Val Phe Ser Glu Ser Phe Thr Lys Thr Glu Leu Leu
197 5 10 15
198 ccc tcg acc ctt gcg gag gac gga cgc tgc cgt ggg ctc ctg gcc gcc 572
199 Pro Ser Thr Leu Ala Glu Asp Gly Arg Cys Arg Gly Leu Leu Ala Ala
200 20 25 30
201 gcc gtg gga acg atg acc gat gat cag gac tgt gct gcg gag ctg gaa 620
202 Ala Val Glv Thr Met Thr Asp Asp Gln Asp Cys Ala Ala Glu Leu Glu

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203	35	40	45		
204	aag gtg gat tct tcc agc gaa gac gga gtt gac gcc aag cca gac cgc			668	
205	Lys Val Asp Ser Ser Ser Glu Asp Gly Val Asp Ala Lys Pro Asp Arg				
206	50	55	60	65	
207	tcc tct atc atc tcc tct att ctc ttg aag aag aag aat gcc tct			716	
208	Ser Ser Ile Ile Ser Ser Ile Leu Leu Lys Lys Lys Arg Asn Ala Ser				
209	70	75	80		
210	gcg ggc ccc gtc agg acc ggc cggt gac cga gtg ccc act tat ctg tac			764	
211	Ala Gly Pro Val Arg Thr Gly Arg Asp Arg Val Pro Thr Tyr Leu Tyr				
212	85	90	95		
213	cgc atg gat ttc cag aag atg ggt aaa tgc atc atc ata aac aac aag			812	
214	Arg Met Asp Phe Gln Lys Met Gly Lys Cys Ile Ile Ile Asn Asn Lys				
215	100	105	110		
216	aac ttc gac aaa gcg aca ggt atg gac gtc cgg aat ggg acg gac aaa			860	
217	Asn Phe Asp Lys Ala Thr Gly Met Asp Val Arg Asn Gly Thr Asp Lys				
218	115	120	125		
219	gat gca ggg gcc ctc ttc aag tgc ttc caa aac ctg ggt ttt gaa gta			908	
220	Asp Ala Gly Ala Leu Phe Lys Cys Phe Gln Asn Leu Gly Phe Glu Val				
221	130	135	140	145	
222	acc gtc cac aat gac tgc tct tgt gca aag atg caa gat ctg ctt aga			956	
223	Thr Val His Asn Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Arg				
224	150	155	160		
225	aaa gcc tct gag gag gac cac agc aac tcg gcc tgc ttc gcc tgc gtc			1004	
226	Lys Ala Ser Glu Glu Asp His Ser Asn Ser Ala Cys Phe Ala Cys Val				
227	165	170	175		
228	ctg ctg agc cac ggg gaa gag gac ctg att tac ggg aaa gat ggc gtg			1052	
229	Leu Leu Ser His Gly Glu Glu Asp Leu Ile Tyr Gly Lys Asp Gly Val				
230	180	185	190		
231	aca ccc ata aag gat ctg aca gct cat ttt agg gga gac cga tgc aaa			1100	
232	Thr Pro Ile Lys Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys				
233	195	200	205		
234	acc ctg tta gag aaa ccc aaa ctc ttc att cag gca tgc cga ggg			1148	
235	Thr Leu Leu Glu Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly				
236	210	215	220	225	
237	acg gag ctc gac gat gga atc cag gct gac tcg ggg ccc atc aac gac			1196	
238	Thr Glu Leu Asp Asp Gly Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp				
239	230	235	240		
240	att gac gct aat ccc cgc aac aag atc ccg gtg gaa gcc gac ttc ctc			1244	
241	Ile Asp Ala Asn Pro Arg Asn Lys Ile Pro Val Glu Ala Asp Phe Leu				
242	245	250	255		
243	ttt gct tac tcc acg gtt cca ggt tat tac tca tgg agg aac cca ggg			1292	
244	Phe Ala Tyr Ser Thr Val Pro Gly Tyr Tyr Ser Trp Arg Asn Pro Gly				
245	260	265	270		
246	aaa ggc tcc tgg ttt gtg cag gcc ctc tgc tcc atc ctg aat gag cat			1340	
247	Lys Gly Ser Trp Phe Val Gln Ala Leu Cys Ser Ile Leu Asn Glu His				
248	275	280	285		
249	ggc aag gac ctc gag atc atg cag atc ctg acc agg gtg aac gac agg			1388	
250	Gly Lys Asp Leu Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg				
251	290	295	300	305	

VERIFICATION SUMMARY

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